



```

DB 181 APTETLAPLRSKFEVFKPKRWODLSMMKKTIGHILAHIOHEVPLECOMVDOVEFD 240
QY 244 KPEVETLAEASVAGUQAMWYKADPNDFYERHRSAAVLPGEEDFYHAAIPGTPYVL 292
DB 241 HPEVGHVATYVAVQAMWYKADPNDFYERHRSAAVLPGEEDFYHAAIPGTPYVL 300
QY 293 NTGPEFKGILKOKKNDLEAGMHDESHLNKYFLNKPTRLISPEYCMYHIGLADIKLV 352
DB 401 NTGPEFKGILKOKKNDLEAGMHDESHLNKYFLNKPTRLISPEYCMYHIGLADIKLV 360
QY 444 KMSWOTKEYNVAVRN 468
DB 461 KMSWOTKEYNVAVRN 476

RESULT 2
QY0065 PRELIMINARY: PKT: 274 AA.
QY0065
AC 01-MAY-2000 (TREMURel. 13, Created)
RT 01-MAY-2000 (TREMURel. 13, Last sequence update)
DT 01-MAY-2000 (TREMURel. 13, Last annotation update)
DE C1S-AL-SPECIFIC ALPHA 1->3 N-ACETYLALACTOSAMINYLTRANSFERASE
(DN FRAGMENT).
GN ABO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX MGI_TaxID=9606;
RN 111
RD SEQUENCE FROM N.A.
RA Yamamoto F.;
RT Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DK EMBL: AF144420; AAD26576.1;
DK FMBL: AF144427; AAD26580.1; JOINED.
KW Transferase.
FT NON_TER 1
FT 274
FT SEQUENCE 274 AA: 31977 MW: 6786627028E2955 CRC64;

Query Match 44.0%; Score 662; DB 4; Length 274;
Best Local Similarity 45.6%; Pred. No. 10-46;
Matches 125; Conservative 50; Mismatches 97; Indels 2; Gaps 2;

QY 94 RPEVVTMKKAPVWEGTYNKAVALDNYAKOKITVGLTFVAVGRTLHYLEPELTSANK 153
DB 1 RKLIVAVTTPMLATVWEGTYNIDLNQFRIQNTTIGLTFALIKYVA-PLKLELTAEK 59
QY 154 HPEVGHVATYVAVQAMWYKADPNDFYERHRSAAVLPGEEDFYHAAIPGTPYVL 213
DB 60 HPEVGHVATYVAVQAMWYKADPNDFYERHRSAAVLPGEEDFYHAAIPGTPYVL 119
QY 214 LGHVDLFCMDYVQVODRKGVETLGSVAVQAMWYKADPNDFYERHRSAAVLPG 273
DB 120 FLSEVDYLVAVDMERDVGVEILTPLEGLHPGFSSREAFYERKPOQAVLPKD 179
QY 274 EGDYFYHAAIPGTPYVNLITGPEFKGILKOKKNDLEAGMHDESHLNKYFLNKPTRL 333
DB 180 EGDYFYHAAIPGTPYVNLITGPEFKGILKOKKNDLEAGMHDESHLNKYFLNKPTRL 219
QY 444 SPEYCMYH-IGLADIKLVKMSWOTKEYNVAVRN 468
DB 240 SPEYCMYH-IGLADIKLVKMSWOTKEYNVAVRN 273

RESULT 3
QY0068 PRELIMINARY: PKT: 274 AA.
QY0068
AC 01-MAY-2000 (TREMURel. 13, Created)
RT 01-MAY-2000 (TREMURel. 13, Last sequence update)

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DB 01-MAY-2000 (TREMURel. 13, Last annotation update)
DE A1-SPECIFIC ALPHA 1->3 N-ACETYLALACTOSAMINYLTRANSFERASE (FRAGMENT).
GN ABO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX MGI_TaxID=9606;
RN 111
RD SEQUENCE FROM N.A.
RA Yamamoto F.;
RT Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DK EMBL: AF134419; AAD26576.1; JOINED.
KW Transferase.
FT NON_TER 1
FT 274
FT SEQUENCE 274 AA: 31977 MW: 7180470668E208A CRC64;

Query Match 32.8%; Score 658; DB 4; Length 274;
Best Local Similarity 45.6%; Pred. No. 2.1e-46;
Matches 124; Conservative 50; Mismatches 98; Indels 2; Gaps 2;

QY 94 RPEVVTMKKAPVWEGTYNKAVALDNYAKOKITVGLTFVAVGRTLHYLEPELTSANK 153
DB 1 RKLIVAVTTPMLATVWEGTYNIDLNQFRIQNTTIGLTFALIKYVA-PLKLELTAEK 59
QY 154 HPEVGHVATYVAVQAMWYKADPNDFYERHRSAAVLPGEEDFYHAAIPGTPYVL 213
DB 60 HPEVGHVATYVAVQAMWYKADPNDFYERHRSAAVLPGEEDFYHAAIPGTPYVL 119
QY 214 LGHVDLFCMDYVQVODRKGVETLGSVAVQAMWYKADPNDFYERHRSAAVLPG 273
DB 120 FLSEVDYLVAVDMERDVGVEILTPLEGLHPGFSSREAFYERKPOQAVLPKD 179
QY 274 EGDYFYHAAIPGTPYVNLITGPEFKGILKOKKNDLEAGMHDESHLNKYFLNKPTRL 333
DB 180 EGDYFYHAAIPGTPYVNLITGPEFKGILKOKKNDLEAGMHDESHLNKYFLNKPTRL 219
QY 334 SPEYCMYH-IGLADIKLVKMSWOTKEYNVAVRN 366
DB 240 SPEYCMYH-IGLADIKLVKMSWOTKEYNVAVRN 273

RESULT 4
QY0591 PRELIMINARY: PKT: 295 AA.
QY0591
AC 01-NOV-1996 (TREMURel. 01, Created)
DT 01-JAN-1999 (TREMURel. 09, Last sequence update)
DT 01-NOV-1999 (TREMURel. 12, Last annotation update)
DE HISTO-BLOOD GROUP A2 TRANSFERASE (FRAGMENT).
GN ABO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN 111
RD SEQUENCE FROM N.A.
RA MEHLING-9239251; PubMed-1520122;
RA Yamamoto F.; McNeill P.D.; Hakomori S.;
RT "Human histo-blood group A2 transferase coded by A2 allele, one of the
RT A subtypes, is characterized by a single base deletion in the coding
RT sequence, which results in an additional domain at the carboxyl
RT terminal."
RL Biochem. Biophys. Res. Commun. 187:366-374(1992).
RN 121
RD SEQUENCE FROM N.A.
RA Yamamoto F.;
RT "Human histo-blood group Abo gene locus alleles."
RT Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DK EMBL: S44054; AAB23167.1;

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Query Match	42.8%	Score 658	DB 4	Length 295
Best Local Similarity	45.38	Prod. No. 2.4e-46		
Matches 124	Conservative 50	Mismatches 98	Indels 2	Gaps

  

FT	SEQUENCE	295 AA	1	MM	0DA33B73906BF5B8	CRC64
DR	EMBL: AF1344422	AAD26577.1	..			
DR	EMBL: AF1344421	AAD26577.1	JOINED.			
MM	Transferase.					
FT	NON_TER					
SO	SEQUENCE	295 AA	1	MM	0DA33B73906BF5B8	CRC64

  

Query	94	RPEVIMIKMKAPVMEGISTYKAVLNDWYAKQKTKVLTFAVAGRYTEHLEFITSANK	153
Db	1	RKQVLVTWPLARLWEGSTENIDLNDFRQNTTIGLTFLFAIKKIYA-FLKLFLEAEK	59
QY	154	HEWGHVHYIYIMWDVSRMDELFLGPIRSFYKFIKIPKRWODISMNRKKTIGEHI	213
Db	60	HEWGHVHYIYVFTDOLAARVRLTIGTGRSLSEYLVAYRWKQVSRMRREIMSDP	119
QY	214	IOHEVDFLCFCDNDVOYQVQDKRGVETLTGESAOLQAMMYKADPNQFTYERREK	273
Db	120	FLSEVDYLVCDVMEPRDHWGFIHPLFCGLTHPGYGSREAFYERKRPQSOAYLP	179
QY	274	EGDYEYHAHIFGCTPTQVLNTQCEFGKILKDKKNDIEAGHDESHLNKFKLLNKP	333
Db	180	EGDPTYLGGFFGGVQVQKRLTRACHQAMAYDQNGIEAVYHDESHLNKILLRKPK	239
QY	334	SPYECWDYH-IGLPADIKLYKMSQTKRYVYVNR	366
Db	240	SPETLMDQQLLGMPALVRLKRLFTAVPRNHQAVRN	273

  

RESULT	5
Q144590	PRELIMINARY; PRI; 354 AA.
ID Q14490	
AC Q14490:	
DT 01-NOV-1996 (TReMBLrel. 01, created)	
DT 01-NOV-1996 (TReMBLrel. 01, last sequence update)	
DT 01-NOV-1999 (TReMBLrel. 12, last annotation update)	
DE HISTO-BLOOD GROUP A TRANSFERASE.	
GN ABO.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
OX NCBI_TaxID:9606;	
XX 111	
RP SEQUENCE FROM N.A.	
RX MEDLINE=95118355; PubMed=7596760;	
RA Bennett E.P.; Steffensen R.; Clausen H.; Weghuis D.O.;	
RA Geurts van Kessel A.;	
RT *Genomic cloning of the human histo-blood group ABO locus.*;	
RL Biochem. Biophys. Res. Commun. 206:118-325(1995).	
RN 121	
RP SEQUENCE FROM N.A.	
RX MEDLINE=95298046; PubMed=7779106;	
RA Bennett E.P.; Steffensen R.; Clausen H.; Weghuis D.O.;	
RA Geurts van Kessel A.;	
RT *Genomic cloning of the human histo-blood group ABO locus.*;	
RL Biochem. Biophys. Res. Commun. 211:347-347(1995).	
RN 131	
RP SEQUENCE FROM N.A.	
RA Yamamoto F.;	
RT *Human histo-blood group ABO gene locus alleles.*;	
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.	
DK EMBL: X84746; CAAS9233.1; .	
DR EMBL: X84747; CAAS9233.1; JOINED.	
DR EMBL: X84748; CAAS9233.1; JOINED.	
DR EMBL: X84749; CAAS9233.1; JOINED.	
DR EMBL: X84750; CAAS9233.1; JOINED.	
DR EMBL: X84751; CAAS9233.1; JOINED.	
DR EMBL: X84752; CAAS9233.1; JOINED.	
DR EMBL: AF1344413; AAD26573.1; .	
DR Transferase	

Seq	SEQUENCE	354 AA	40950 MW	C344EF584F177134 CIRC64
QY	Query Match	32.8%	Score 658	DB 4
	Best Local Similarity	45.3%	Pred. No. 3e-46	
	Matches 124	Conservative 50	Mismatches 98	Indels 2
QY	94 RREYVMTKRPVYVMECTSYNKAVIDNYAKQITVGLTVAVGCHYIEHYHLEPFTISANK	153		
DB	81 KRQVLYVTPMLAPDIWECTSFNDINDEORLQNTTIGLVFAIKRYVA-FLKPLFTAK	139		
QY	154 HFMVGHPIVFLYIMVDVSRMPLIEGLPRSEFVKIKPEKRMODISNMKMTIGEHIVAH	213		
DB	140 HFMVGHRRHYVFLTDQLAAPRVTLTGTRQSLVLEVRATKKNQDVSMRMEMISPECKR	199		
QY	214 IQHEVDLEFCMDVDVDFQDKFQVETLIGESVAOLQAWMYKADNPFTYERKESAAVIFPG	273		
DB	200 FLSEVDYLVCVDDVDFEPRDHVGEVLLPLFTGLHPGFSSREAEFTYERKPOSAVIFPD	259		
QY	274 EDDFYHNAIFGCTPTQVUNITQEGCFKILKKKKNDIEQWIDESHUNKYLLNKPTRL	333		
DB	260 EDDFYHICFGFCGSQVEQVGRILRACHQAMVDAQANGIAVWHDESHUNKYLLNKPTRL	319		
QY	334 SPEYCMQYH-IGLPADIKLVKMSMOTKEVNVRN	366		
DB	320 SPEYIMDQQLGMPRAVLKRLRTAIPKKNQAVRN	353		
RESULT	6			
ID	Q9U063	PRELIMINARY	PRT:	274 AA.
AC	Q9U063			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DR	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DE	01-MAY-2000 (TREMBLrel. 13, Last annotation update)			
GN	B(A)-SPECIFIC ALPHA 1->3 GALACTOSYLTRANSFERASE (FRAGMENT1).			
OS	ABO.			
OC	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RA	SEQUENCE FROM N.A.			
RP	Yamamoto F.;			
RT	"Human histo-blood group ABO gene locus alleles.";			
RI	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF134433; AAD26583.1; J01NEO.			
KM	Transferase; AAD26583.1; JOINED.			
FT	NON_TER	1		
FT	NON_TER	1		
SO	SEQUENCE	274 AA;	31894 MW;	65F322EFA302BFA73 CRC64;
QY	Query Match	32.7%	Score 656	DB 4
	Best Local Similarity	45.6%	Pred. No. 3.1e-46	
	Matches 125	Conservative 48	Mismatches 95	Indels 2
QY	94 RREYVMTKRPVYVMECTSYNKAVIDNYAKQITVGLTVAVGCHYIEHYHLEPFTISANK	153		
DB	1 KRQVLYVTPMLAPDIWECTSFNDINDEORLQNTTIGLVFAIKRYVA-FLKPLFTAK	59		
QY	154 HFMVGHPIVFLYIMVDVSRMPLIEGLPRSEFVKIKPEKRMODISNMKMTIGEHIVAH	213		
DB	60 HFMVGHRRHYVFLTDQLAAPRVTLTGTRQSLVLEVRATKKNQDVSMRMEMISPECKR	119		
QY	214 IQHEVDLEFCMDVDVDFQDKFQVETLIGESVAOLQAWMYKADNPFTYERKESAAVIFPG	273		
DB	120 FLSEVDYLVCVDDVDFEPRDHVGEVLLPLFTGLHPGFSSREAEFTYERKPOSAVIFPD	179		
QY	274 EDDFYHNAIFGCTPTQVUNITQEGCFKILKKKKNDIEQWIDESHUNKYLLNKPTRL	333		
DB	180 EDDFYHMGFFGGSQVEQVGRILRACHQAMVDAQANGIEVWHDESHUNKYLLNKPTRL	239		



Query Match 32.6%; Score 655; DB 4; Length 274;  
 Best Local Similarity 45.3%; Pred. No. 3.8e-46;  
 Matches 124; Conservative 49; Mismatches 99; Indels 2; Gaps 2;

QY 94 REPVYMTKMKAPVVEGTYNNKAVLDNYAKOKITVGLVFAVNGRIEHLLEFLTSANK 153  
 DB 1 RKDVLAVTFLWALVEGTFNIDILNEQFLQNTTIGLVFAIKRYVA-FLKLETAER 59  
 QY 154 HFWGHPVIFYIMVDVDSMPLELGLPLRSFVKYIKPEKRMODISMNMKRTIGEHIVAH 213  
 DB 60 HFWGHPVIFYIMVDVDSMPLELGLPLRSFVKYIKPEKRMODISMNMKRTIGEHIVAH 119  
 QY 214 IOHEVDLFECMDVQVFOKPGVEITLGEVVAOLQAMWYKADPNFTYERKESAAVIFPG 273  
 DB 120 FLSEVDYLCVDMFEPHVGVEITLPGTLHPGFGSSRAEFTYERROQAVIPKD 179  
 QY 274 EGDFFYHAAIFGCTPTQVNTIOECFGKILKDKNDIEQMHDESHLNKYFLNKPFTKIL 333  
 DB 180 EGDFFYLCGFGGSGVEQVORLTRACHQAMVDOANGIEAVWHDESHNLNKPFTKIL 239  
 QY 334 SPEYCMDYH-IGLPADIKLVKMSWOTKEYNVN 366  
 DB 240 SPEYMDQQLGMPAVLRKRLRFTAVPKNHQAVRN 273  
 RESULT 10  
 Q90IKR1 PRELIMINARY; PRT; 274 AA.  
 AC Q90IKR1:  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)  
 DE ABO GLYCOSYLTRANSFERASE (FRAGMENT).  
 GN ABO.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RA YIP S.P.;  
 RT \*Single-tube multiplex PCR-SSCP analysis distinguishes seven common  
 RT ABO alleles and readily identifies new alleles.\*;  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF182746; AAF07060.1; -;  
 DR EMBL: AF182745; AAF07060.1; JOINED.  
 DR InterPro: IPR002369; -;  
 DR ProDom: P0001811; -; 1;  
 DR Transferrase.  
 KW 1  
 FT NON\_TER 1  
 FT NON\_TER 274  
 SU SEQUENCE 274 AA; 32020 MW; 11F74AC48954AB6 CRC64;

Query Match 32.6%; Score 655; DB 4; Length 274;  
 Best Local Similarity 45.3%; Pred. No. 3.8e-46;  
 Matches 124; Conservative 49; Mismatches 99; Indels 2; Gaps 2;

QY 94 REPVYMTKMKAPVVEGTYNNKAVLDNYAKOKITVGLVFAVNGRIEHLLEFLTSANK 153  
 DB 1 RKDVLAVTFLWALVEGTFNIDILNEQFLQNTTIGLVFAIKRYVA-FLKLETAER 59  
 QY 154 HFWGHPVIFYIMVDVDSMPLELGLPLRSFVKYIKPEKRMODISMNMKRTIGEHIVAH 213  
 DB 60 HFWGHPVIFYIMVDVDSMPLELGLPLRSFVKYIKPEKRMODISMNMKRTIGEHIVAH 119  
 QY 214 IOHEVDLFECMDVQVFOKPGVEITLGEVVAOLQAMWYKADPNFTYERKESAAVIFPG 273  
 DB 120 FLSEVDYLCVDMFEPHVGVEITLPGTLHPGFGSSRAEFTYERROQAVIPKD 179  
 QY 274 EGDFFYHAAIFGCTPTQVNTIOECFGKILKDKNDIEQMHDESHLNKYFLNKPFTKIL 333

DB 180 EGDFFYLCGFGGSGVEQVORLTRACHQAMVDOANGIEAVWHDESHNLNKPFTKIL 239  
 QY 334 SPEYCMDYH-IGLPADIKLVKMSWOTKEYNVN 366  
 DB 240 SPEYMDQQLGMPAVLRKRLRFTAVPKNHQAVRN 273

RESULT 11  
 Q9ET32 PRELIMINARY; PRT; 348 AA.  
 AC Q9ET32:  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)  
 DE N-ACETYLGLYCOSAMINYLTRANSFERASE A BLOOD GROUP-LIKE ENZYME.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-BDIX; TISSUE-STOMACH;  
 RA Valde B., Marionneau S., Calileu-Thomas A.L., Bouhours D.,  
 RA Le Pendu J.;  
 RT \*Rat N-acetylglucosaminyltransferase A blood group-like enzyme.\*;  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF264018; AAF74758.2; -;  
 DR Transferrase.  
 KW 1  
 SU SEQUENCE 348 AA; 40375 MW; FC5E572B10ED7B3 CRC64;

Query Match 32.6%; Score 654; DB 11; Length 348;  
 Best Local Similarity 45.3%; Pred. No. 6.3e-46;  
 Matches 124; Conservative 48; Mismatches 100; Indels 2; Gaps 2;

QY 94 REPVYMTKMKAPVVEGTYNNKAVLDNYAKOKITVGLVFAVNGRIEHLLEFLTSANK 153  
 DB 76 RNDVLAVTFLWALVEGTFNIDILNEQFLQNTTIGLVFAIKRYVA-FLKLETAER 134  
 QY 154 HFWGHPVIFYIMVDVDSMPLELGLPLRSFVKYIKPEKRMODISMNMKRTIGEHIVAH 213  
 DB 135 HFWGHPVIFYIMVDVDSMPLELGLPLRSFVKYIKPEKRMODISMNMKRTIGEHIVAH 194  
 QY 214 IOHEVDLFECMDVQVFOKPGVEITLGEVVAOLQAMWYKADPNFTYERKESAAVIFPG 273  
 DB 195 IOHEVDYLCVDMFEPHVGVEITLPGTLHPGFGSSRAEFTYERROQAVIPKD 254  
 QY 274 EGDFFYHAAIFGCTPTQVNTIOECFGKILKDKNDIEQMHDESHLNKYFLNKPFTKIL 333  
 DB 255 EGDFFYAGGFGGSGVEVHNLTRACHQAMVDOANGIEAVWHDESHNLNKPFTKIL 314  
 QY 334 SPEYCMDYH-IGLPADIKLVKMSWOTKEYNVN 366  
 DB 315 SPEYMDQQLGMPAVLRKRLRFTAVPKNHQAVRN 348

RESULT 12  
 Q9TNT5 PRELIMINARY; PRT; 274 AA.  
 AC Q9TNT5:  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, last annotation update)  
 DE ABO GLYCOSYLTRANSFERASE (FRAGMENT).  
 GN ABO.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN 11  
 RP SEQUENCE FROM N.A.



DT	01-MAY-2000	(TEMBLrel. 13, Created)	
DT	01-MAY-2000	(TEMBLrel. 13, last sequence update)	
DT	01-MAY-2000	(TEMBLrel. 13, last annotation update)	
DE	O-SPECIFIC ALPHA 1->3 N-ACETYLGLACTOSAMINYLTRANSFERASE (FRAGMENT)		
GN	AAO.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
OX	NCBI_TaxId=9606;		
RN	{1}		
RP	SEQUENCE FROM N.A.		
RA	Yamamoto F.;		
RI	"Human histo-blood group ABO gene locus alleles.";		
RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL:	AF134440;	AAD26584.1;
DR	EMBL:	AF134439;	AAD26584.1; JOINED.
KW	Transferase.		
FT	NONTER	1	1
FT	NONTER	274	274
SO	SEQUENCE	274 AA;	31961 MW; 06d300e8022af4b6 CRC64;

[illegible]

Search completed: November 5, 2001, 15:22:21  
Job time: 8384 sec

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